Amendments to the Specification

Please replace the paragraph at page 10, lines 7-15 with the following paragraph:

FIGURE 14. Potential functional domains of TARP. (A) TARP contains a potential leucine zipper motif and phosphorylation sites. A potential leucine zipper motif is indicated with boxed leucines followed by a basic region that is underlined. cAMP- and cGMP-dependent protein kinase phosphorylation sites (amino acids 46-49 and 55-58, see SEQ ID NO: 14) and protein kinase C phosphorylation sites (amino acids 19-21 and 20-22, see SEQ ID NO: 15) are outlined. (B) Protein sequence comparison of TARP with Tup1 . Amino acids sequences for TARP (42-57, SEQ ID NO: 16), *Dictyostelium dicoideum* Tup1 (dTup1, 521-536, SEQ ID NO: 17) and *Saccharomyces cerevisiae* Tup1 (yTup1, 626-660, SEQ ID NO: 18) are shown. Conserved residues are boxed.

Please replace the paragraph at page 13, lines 9-28 with the following paragraph:

To determine if TARP shares homology with any known proteins, we performed a protein BLAST search against ~~GenBank~~ GENBANK® (database). This search indicated that the amino acid sequence of TARP shares some homology to *Dictyostelium dicoideum* Tup1 (~~GenBank~~ GENBANK® (database) accession no. AAC29438) and *Saccharomyces cerevisiae* Tup1 (Williams, F. E. *et al.*, *Mol. Cell. Biol.* 10:6500-6511 (1990)) (Figure 14B). Yeast Tup1 is normally found in a complex with Cyc8(Ssn6) and is required for transcriptional repression of genes that are regulated by glucose, oxygen and DNA damage (Tzamarias, D. *et al.*, *Genes Dev.* 9:821-831 (1995)). Neither Cyc8(Ssn6) nor Tup1 binds DNA, but each acts as a part of a corepressor complex through interactions with specific DNA-binding proteins such as α2, Mig1, Rox1 and a1 (Tzamarias, D. *et al.*, *Genes Dev.* 9:821-831 (1995)). The C'-terminal half of Tup1 contains six repeats of a 43-amino acid sequence rich in aspartate and tryptophan, known as WD-40 or β-transducin repeats (Williams, F. E. *et al.*, *Mol. Cell. Biol.* 10:6500-6511 (1990); Fong, H. K. *et al.*, *Proc. Natl. Acad. Sci. USA* 83:2162-2166 (1986)). WD-40 repeats have been identified in many proteins and play a role in protein-protein interactions. Importantly, Tup1 has been shown to interact with α2 through two of its WD-40 repeats (Komachi, K. *et al.*, *Genes Dev.*

8:2857-2867 (1994)). It is interesting to note that TARP shares homology with the fifth WD-40 repeat of Tup1 (Figure 14B ~~7C~~). Because TARP is a nuclear protein, its homology with Tup1 suggests that TARP is a member of a functional nuclear protein complex involved in transcriptional regulation.

Please replace the paragraph at page 42, line 31 to page 43, lines 18 with the following paragraph:

RNA dot blot (RNA master blot, Clontech, Palo Alto, CA), and Northern blot (MTN, Clontech, Palo Alto, CA), were performed on a variety of human tissues. Northern blot was also performed on mRNA from prostate adenocarcinoma cell lines, LNCaP and PC-3 (ATCC, Rockville, MD). Isolation of poly(A) RNA was carried out using ~~the~~ FASTTRACK™ ~~FastTrack~~ (kit) (InVitrogen, Carlsbad, CA). RNA was electrophoresed on a 1% agarose gel and transferred to nylon-based membranes (GENESCREEN PLUS™ ~~GeneScreen Plus~~, DuPont, Wilmington, DE), according to established procedures. Ausubel, *supra*. A cDNA probe specific for the untranslated 3' end (3' UTR) of the TCRγ transcript was made from EST plasmid ng79d11 (Genome Systems, St. Louis, MO). A probe specific for the constant domain of the TCRγ transcript (TCR Cγ) was made from LNCaP cDNA and a probe for the constant domain of the TCRδ transcript (TCR Cδ) was made from a TCRδ plasmid. A human β-actin probe was used as a quantity control of the mRNA preparations. Probes were labeled with ^{32}P by random primer extension (Lofstrand Labs Limited, Gaithersburg, MD) to a specific activity of 1 μCi/ng. The RNA membranes were blocked for 2 hours at 45° C in hybridization solution containing 50% formamide (Hybrisol I, Oncor, Gaithersburg, MD) and then probed for 15 hours at 45° C with 20 μCi cDNA in 20 ml hybridization solution. The membranes were washed twice for 15 minutes at room temperature in 2xSSC/0.1%SDS and twice for 20 minutes at 55-65° C in 0.1%SSC/0.1%SDS. The membranes were exposed to an imaging film (X-OMAT™, Kodak, Rochester, NY) at -80° C before development.

Please replace the paragraph at page 47, lines 3-11 with the following paragraph:

TCR γ-chain protein is normally co-expressed with the TCR δ-chain protein. Since the TCRγ gene is transcriptionally active in human prostate, we went on to analyze the transcriptional activity of the TCRγ gene. The dbEST was analyzed (~~http://www.ncbi.nlm.nih.gov/BLAST~~ on the NCBI website) using the TCRδ transcript nucleotide sequence. ESTs from prostate cDNA libraries did not match any part of the TCR δ-chain transcript. Furthermore, Northern blot analysis did not detect any prostate expression of TCRδ mRNA, Figure 3B (lane 3). We conclude that the TCRδ gene is silent in prostate. As expected, TCRδ transcripts are expressed in spleen, thymus and blood leukocytes, Figure 3B.

Please replace the paragraph found at page 59, line 25-35 with the following paragraph:

The TARP antibody recognizes a doublet in prostate and breast nuclear extracts (Figure 13A). The faster 7 kDa band comigrates with the His-TARP recombinant protein, while the weaker band runs at a larger molecular weight. One possible explanation for the 9 kDa band is post-translational modifications. To determine if TARP contains any known post-translational modification sites, we analyze the TARP amino acid sequence using the PROSITE program of the *Swiss Institute of Bioinformatics* ExPASy proteomics server [(~~http://www.expasy.ch~~) available on the internet] (Appel, R.D. *et al.*, *Trends Biochem. Sci.* **19**:248-260 (1994); Hofmann, K *et al.*, *Nucleic Acids Res.* **27**:215-219 (1999)). As shown in Figure 14A, many potential phosphorylation sites were found including cAMP- and cGMP-dependent protein kinase phosphorylation sites (RRAT (SEQ ID NO:32) and RRGT (SEQ ID NO:33)) and

Please replace the paragraph found at page 59, lines 4-24 with the following paragraph:

To determine if TARP shares homology with any known proteins, we performed a protein BLAST search against ~~GenBank~~ GENBANK® (database). This search indicated that the amino acid sequence of TARP shares some homology to *Dictyostelium dicoideum* Tup1 (~~GenBank~~ GENBANK® (database) accession no. AAC29438) and *Saccharomyces cerevisiae* Tup1 (Williams, F. E. *et al.*, *Mol. Cell. Biol.* **10**:6500-6511 (1990)) (Figure ~~7C~~ 14B). Yeast

Tup1 is normally found in a complex with Cyc8(Ssn6) and is required for transcriptional repression of genes that are regulated by glucose, oxygen and DNA damage (Tzamarias, D. *et al.*, *Genes Dev.* **9**:821-831 (1995)). Neither Cyc8(Ssn6) nor Tup1 binds DNA, but each acts as a part of a corepressor complex through interactions with specific DNA-binding proteins such as α2, Mig1, Rox1 and **a**1 (Tzamarias, D. *et al.*, *Genes Dev.* **9**:821-831 (1995)). The C'-terminal half of Tup1 contains six repeats of a 43-amino acid sequence rich in aspartate and tryptophan, known as WD-40 or β-transducin repeats (Williams, F. E. *et al.*, *Mol. Cell. Biol.* **10**:6500-6511 (1990); Fong, H. K. *et al.*, *Proc. Natl. Acad. Sci. USA* **83**:2162-2166 (1986)). WD-40 repeats have been identified in many proteins and play a role in protein-protein interactions. Importantly, Tup1 has been shown to interact with α2 through two of its WD-40 repeats (Komachi, K. *et al.*, *Genes Dev.* **8**:2857-2867 (1994)). It is interesting to note that TARP shares homology with the fifth WD-40 repeat of Tup1 (Figure 14B ~~7C~~). Because TARP is a nuclear protein, its homology with Tup1 suggests that TARP may be a member of a functional nuclear protein complex involved in transcriptional regulation. Therefore, it is necessary to identify TARP-interacting proteins in order to determine its function.